

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: November 5, 2001, 15:19:11 : Search time 60.22 Seconds

(without alignments)
465.497 Million cell updates/sec

Title: US-09-593-316-4

Sequence: 1 MNVKGKVIILSMVLVSTIVV.....IKLVKSMQTKREYNVKNNV 368

Scoring table: BiOSUM62
Gapop 10.0 / Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR68:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|----------------------------|
| 1 | 2008 | 100.0 | 368 | 2 | A44785 N-acetyllactosamin |
| 2 | 1717.5 | 85.5 | 371 | 2 | A45883 alpha-1,3-galactos |
| 3 | 1701 | 84.7 | 376 | 2 | A56480 N-acetyllactosamin |
| 4 | 1524.5 | 75.9 | 371 | 2 | I49698 alpha-1,3-galactos |
| 5 | 1476.5 | 73.5 | 394 | 2 | A34417 alpha-1,3-mannosyl |
| 6 | 658 | 32.8 | 295 | 2 | PC1120 fucosylgalactose a |
| 7 | 656 | 32.7 | 353 | 1 | A34933 fucosylgalactose a |
| 8 | 626 | 31.2 | 347 | 2 | JC6126 globoside alpha-N- |
| 9 | 456 | 22.7 | 189 | 2 | PC1168 histo-blood group |
| 10 | 453.5 | 22.6 | 189 | 2 | PC1165 fucosylgalactose a |
| 11 | 452.5 | 22.5 | 189 | 2 | PC1173 histo-blood group |
| 12 | 450.5 | 22.4 | 189 | 2 | PC1166 histo-blood group |
| 13 | 449.5 | 22.4 | 189 | 2 | PC1169 histo-blood group |
| 14 | 449.5 | 22.4 | 189 | 2 | PC1170 histo-blood group |
| 15 | 449.5 | 22.4 | 189 | 2 | PC1171 histo-blood group |
| 16 | 447.5 | 22.3 | 189 | 2 | PC1172 histo-blood group |
| 17 | 118 | 5.9 | 26 | 2 | A39769 N-acetyllactosamin |
| 18 | 115.5 | 5.8 | 505 | 2 | A32261 agarase (EC 3.2.1. |
| 19 | 102.5 | 5.1 | 559 | 2 | A45987 polypeptide N-acet |
| 20 | 101.5 | 5.1 | 559 | 2 | JC4223 glutamate--ammonia |
| 21 | 97.5 | 4.9 | 448 | 2 | I45145 hypotheical prote |
| 22 | 97 | 4.8 | 3724 | 2 | T18427 collagen alpha 1(I) |
| 23 | 94.5 | 4.7 | 585 | 2 | C78634 conserved hypotet |
| 24 | 94.5 | 4.7 | 1418 | 2 | T45467 genome polypeptid |
| 25 | 94.5 | 4.7 | 1520 | 2 | B82274 hypotheical prote |
| 26 | 94.5 | 4.7 | 2410 | 1 | J01948 hypotheical prote |
| 27 | 94 | 4.7 | 278 | 2 | F86679 hypotheical prote |
| 28 | 94 | 4.7 | 865 | 2 | E84718 hypotheical prote |
| 29 | 93 | 4.6 | 408 | 2 | H64513 |

| | | | | | |
|----|------|-----|------|---|----------------------------|
| 30 | 92.5 | 4.6 | 1487 | 1 | CGH6C collagen alpha 1(I) |
| 31 | 90 | 4.5 | 708 | 1 | TVVPT4 large T antigen - |
| 32 | 89.5 | 4.5 | 478 | 2 | H64970 mannose-1-phosphat |
| 33 | 89.5 | 4.5 | 2054 | 2 | T07584 hypotheical prote |
| 34 | 89 | 4.4 | 688 | 1 | TVVPTJ large T antigen - |
| 35 | 89 | 4.4 | 1827 | 1 | 00HU sucrose alpha-4-ep |
| 36 | 88.5 | 4.4 | 288 | 1 | CGH6C collagen alpha 1(I) |
| 37 | 88.5 | 4.4 | 478 | 2 | A85831 mannose-1-phosphat |
| 38 | 88.5 | 4.4 | 483 | 2 | T05168 protein kinase f41 |
| 39 | 88.5 | 4.4 | 708 | 2 | S53411 hypotheical prote |
| 40 | 88.5 | 4.4 | 788 | 2 | A71076 hypotheical prote |
| 41 | 88.5 | 4.4 | 1419 | 2 | A41182 collagen alpha 1(I) |
| 42 | 88.5 | 4.4 | 1487 | 2 | B41182 collagen alpha 1(I) |
| 43 | 88 | 4.4 | 533 | 2 | T41382 acetamidase - tiss |
| 44 | 88 | 4.4 | 567 | 2 | C64478 hypotheical prote |
| 45 | 88 | 4.4 | 609 | 2 | T14759 hypotheical prote |

ALIGNMENTS

RESULT 1
A44785
N-acetyllactosamine 3-alpha-galactosyltransferase (EC 2.4.1.124) - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 19-Mar-1993 #sequence_travis19-Mar-1993 #textl-change 29-Sep-1993
C:Accession: A44785
R:Joziassse, D.H.; Shaper, J.H.; Van den Eljnden, D.H.; Van Tancu, A.J.; Shaper, N.L.
J. Biol. Chem. 264, 14290-14297, 1989
A:Title: Bovine alpha1-3-galactosyltransferase: isolation and characterization of a
A:Reference number: A44785; MUID:89340543
A:Accession: A44785
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-368 <J02>
A:Cross-references: GB:J04989; NID:q163123; PID:AAA30558.1; PID:q163124
C:Superfamily: histo-blood group 1 transferase
C:Keywords: glycosyltransferase; hexosyltransferase; transmembrane protein

| | | | | |
|-----------------------|-----------------|-------------------------------------------------------------|-----------|-------------|
| Query Match | 100.0% | Score 2008: | DB 2: | length 368: |
| Best Local Similarity | 100.0% | Pred. No. 6.4e-161: | | |
| Matches 368: | Conservative 0: | Mismatches 0: | Indels 0: | Gaps 0: |
| QY | 1 | MNVKGKVIILSMVLVSTIVVENEYIHSFEGSLFWINPSRNHPVGGSTIQKGMWLPMPFN | 60 | |
| DB | 1 | MNVKGKVIILSMVLVSTIVVENEYIHSFEGSLFWINPSRNHPVGGSTIQKGMWLPMPFN | 60 | |
| QY | 61 | GYNEDGDINEEKEORNEDESKLKISDMFNPRKREVVTKMKAPVWVEGTYNRAVDN | 120 | |
| DB | 61 | GYNEDGDINEEKEORNEDESKLKISDMFNPRKREVVTKMKAPVWVEGTYNRAVDN | 120 | |
| QY | 121 | YAAKKTIVGLTVFVAGYIIEHYLEFPTSANKHFMVAGPVIFVIMVDVSRMPLIELGP | 180 | |
| DB | 121 | YAAKKTIVGLTVFVAGYIIEHYLEFPTSANKHFMVAGPVIFVIMVDVSRMPLIELGP | 180 | |
| QY | 181 | LRSFVEFKIKPEKRMODISMKMKKTIGENIVANIQHEDVPLFCMDVDPVDFDKFVETIG | 240 | |
| DB | 181 | LRSFVEFKIKPEKRMODISMKMKKTIGENIVANIQHEDVPLFCMDVDPVDFDKFVETIG | 240 | |
| QY | 241 | ESVALDQMMVYKADPNDFTEERKESAAVIRGEGEDFYHNAIFGSGTVOVLINTOEGFK | 300 | |
| DB | 241 | ESVALDQMMVYKADPNDFTEERKESAAVIRGEGEDFYHNAIFGSGTVOVLINTOEGFK | 300 | |
| QY | 301 | GLLKKNKNIIEAQMDESHLNKPYLNKPTKIISPEYQWDNIGIPADIKIVKMSWQTK | 360 | |
| DB | 301 | GLLKKNKNIIEAQMDESHLNKPYLNKPTKIISPEYQWDNIGIPADIKIVKMSWQTK | 360 | |
| QY | 361 | YVNVVNNV 368 | | |
| DB | 361 | YVNVVNNV 368 | | |

RESULT 2

146583

alpha 1,3-galactosyltransferase - pig

cl:Species: Sus scrofa domestica (domestic pig)

cl:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 29-Sep-1999

cl:Accession: 146583

cl:Strahan, K.M.; Gu, F.; Proctor, A.F.; Gustavsson, L.; Andersson, B.; Gustafsson, K.

ImmuneGenetics 41, 101-105, 1995

cl:Title: cDNA sequence and chromosome localization of pig alpha 1,3 galactosyltransferase

cl:Reference number: 146583; MIMID:95104914

A:Accession: 146583

A:Status: preliminary; translated from CH/EMBL/DBEM

A:Molecule type: mRNA

A:Residues: 1 371 c-STR

A:Cross-references: CH:146152; NID:q642635; PID:AAA7558.1; PID:q642636

cl:Genetics:

A:Gene: GFPA1

cl:Superfamily: histo blood group I transferase

| | | | | |
|-----------------------|------------------|----------------------|-----------|-------------|
| Query Match | 85.5%; | Score 1717.5; | DB 2; | Length 371; |
| Best Local Similarity | 84.1%; | Prod. NO. 1,600,136; | | |
| Matches 343; | Conservative 40; | Mismatches 24; | Indels 5; | Gaps 3 |

[illegible]

RESULT 4
 A56480
 N-acetylglucosaminide alpha 1,3-galactosyltransferase (EC 2.4.1.151) ~ marmoset
 C:Species: Callithrix sp.
 C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 29-Sep-1999
 C:Accession: A56480
 R:Reimann, T.R.; Mothert, B.A.; Anaraki, F.; Gallili, D.
 C:Title: Defining the minimal size of catalytically active primate alpha1,3-galactosyltransferase
 A:Accession: A56480
 A:Accession: A56480
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Accession: 1-476 + GEN
 A:Cross_references: GEN:571444; NID:q95H051; P1DN:AAB31587.1; P1D:q95H052
 A:Notes: authors translated the codon CTG for residue 251 as Ser
 C:Superfamily: histone blood group 1 transferase
 C:Keywords: glycosyltransferase; hexosyltransferase; transmembrane protein

| | | | | |
|-----------------------|-----------------|---------------------|----------|------------|
| Query Match | 84.7% | Score 1701 | DB 2 | Length 376 |
| Best local Similarity | 81.9% | Pred. No. 3, 90-155 | | |
| Matches 308 | Conservative 33 | Mismatches 27 | Indels 8 | Gaps 2 |

| | | | | | | | | | |
|----|-----|----------------------------|---------------|--------------|---------|---------------|----------|------------|-----|
| QY | 1 | MNVGKVLISMLVSVTVVFWWEY | INSPESCLFW | INSPNDPEVGSS | LQGMW | PRMFWNN | 60 | | |
| Db | 1 | MNVGKVLISMLVSVTVVFWWEY | INSPESCLFW | INSPNDPEVGSS | LQGMW | PRMFWNN | 60 | | |
| QY | 61 | GYH-----EHGDDI---- | NEEKPOBNEDESK | KLSIDWNP | PKRFVVT | MTKKNKAPVWEET | 112 | | |
| Db | 61 | GYH-----EHGDDI---- | NEEKPOBNEDESK | KLSIDWNP | PKRFVVT | MTKKNKAPVWEET | 112 | | |
| QY | 113 | YNRAVLNNYAKOKITVGLTVFAVGRT | IEHYDEEEL | SARKHBMVGHV | IFY | IMVADVSK | 172 | | |
| Db | 121 | YNRAVLNNYAKOKITVGLTVFAVGRT | IEHYDEEEL | SARKHBMVGHV | IFY | IMVADVSK | 172 | | |
| QY | 173 | MDLFEIGLISFSEKPKFKT | PERKROWD | ISMBHKK | TL | GENIVAH | LOHEVDPL | PCMDVDVPOD | 212 |
| Db | 181 | APFLIEIGLISFSEKPKFKT | PERKROWD | ISMBHKK | TL | GENIVAH | LOHEVDPL | PCMDVDVPOD | 240 |
| QY | 243 | KPGVHTLGEASAOLQAWMYKAD | INDP | TYERRKBSAAV | IP | PEKQIDPY | HAA | PEGTPTQVL | 292 |
| Db | 241 | HEGVEHTLGEASAOLQAWMYKAD | INDP | TYERRKBSAAV | IP | PEKQIDPY | HAA | PEGTPTQVL | 300 |
| QY | 293 | NITQCHCEKGLLKDKKKN | IEADWDESH | LNKFT | KL | ISPEYCMDYH | GH | PAIDIKV | 352 |
| Db | 301 | NITQCHCEKGLLKDKKKN | IEADWDESH | LNKFT | KL | ISPEYCMDYH | GH | PAIDIKV | 360 |
| QY | 353 | KMSWQTKREYNVNRNV | 368 | | | | | | |
| Db | 361 | KLSMOTKREYNVNRNV | 376 | | | | | | |

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RESULT      4
149698
alpha-1,3-galactosyltransferase - mouse
C1:Species: Mus musculus (house mouse)
C1:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 29-Sep 1999
C1:Accession: 149698
R:Joziasse, D.H.; Shaper, N.L.; Kim, D.; van der Eijnden, D.H.; Shaper, J.H.
J. Biol. Chem. 267, 5534-5541, 1992
A:Title: Murine alpha-1,3-galactosyltransferase: A single gene locates four
A:Reference number: A2117; M010:92184813
A:Accession: 149698
A:Status: preliminary; translated from GH/EM01/MD03
A:Molecule type: mRNA
A:Cross-references: GH:M05153; NID:q193563; FIDN:AA3771.1; PID:q457142
C1:Genetics:
A:Gene: Gata-1
C1:Superfamily: histo-blood group 1 transferase

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| Query | Match | Score | 1524_5 | 16_2 | Length | 371 |
|-----------------------|-------|-------------------------------------------------------------------|----------|------------|--------|------|
| Query | Match | Score | 1524_5 | 16_2 | Length | 371 |
| Best Local Similarity | 73.6% | Prod. No. | 2_50-120 | | | |
| Matches | 273 | Conservative | 44 | Mismatches | 512 | Gaps |
| QY | 1 | MNVRGKAVLLSMILVSTVATVIVFWEYIHSPESGLFWINPNSNDPVGSSILQCKRMIDLPRWFNN | 60 | | | |
| DB | 1 | MMVKCKAVLLMLLVSTVVVVFWFVYVNSPLDSGLAWYHETIPVGNRNRQKMMFSPWFNN | 60 | | | |
| QY | 61 | GYN--EEDQDINBEKROREDE-SKLSISIMNPDKRPDVPVIMTKAKAVVMVNGEYINRAV | 117 | | | |
| DB | 61 | GHSTSDQVNEGCRKREGKRGKQDRIEHLQVMDQINPKNKRGVLTIVTWKATLVNKGITDPAAL | 120 | | | |
| QY | 118 | LDNYAKRKITVGLTVFAVGKYLEHYITFEELTSANKHINVCNIVATIPMDVDSRMLILE | 177 | | | |
| DB | 121 | LEKYVATQKLTGGLTVFAVGKYLEHLEDFDSADMYFVAGKVLIPYVMLDITSRKVVH | 180 | | | |
| QY | 178 | LCPIISFKFEKYLKPKRPMQDLSNMRKRTIGENIVAHIGHVPLFCMDVQVQJQFGEV | 237 | | | |
| DB | 181 | LNPLNLSLVFELIKSEKRWQDLSMKRKRTILEHLLLAHIGHVPLFCMDVQVQJQFGEV | 240 | | | |

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QY 218 TLGSGVALQAMWKKADPNDFYERRKESAVIFPGCEDFYHAAIFGCTGYOANTIOE 297
Db 241 TLGQVALQAMWKKASPEKTYTERRELSAAVIFPGCEDFYHAAIFGCTGYHINTLRE 300
QY 298 CFKGLKDKRKNDIEAQMDESHLNKYPFLNKPRTKLSPCYCMDYHIGPADIKLVKMSQ 357
Db 301 CFKGLIDQKKHNDIEAQMDESHLNKPYFLNKNPRTKLSPCYCMDYDQIGLPSDIKSVKAWQ 360
QY 358 TKEYNVVARNV 368
Db 361 TKEYNLVRNV 371

RESULT 5
A34417
alpha-1,3-mannosyl-glycoprotein beta-1,4-N-acetylglucosaminyltransferase (EC 2.4.1.145)
C:Species: Mus musculus (house mouse)
C:Date: 15-Jun-1990 #sequence_revision 15-Jun-1990 #text_change 29-Sep-1999
C:Accession: A34417
R:Larsen, R.D.; Rajan, V.P.; Ruff, M.M.; Kukowska-Latallo, J.; Cummings, R.D.; Lowe, J.E.
Proc. Natl. Acad. Sci. U.S.A. 86, 8227-8231, 1989
A:Title: Isolation of a cDNA encoding a murine UDPgalactose:beta-D-galactosyl-1,4-N-acetyl-
A:Reference number: A34417; MUID:90046769
A:Accession: A34417
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-394 <LRR>
A:Cross-references: GB:M6925; NID:q193419; PIDN:AAA37657.1; PID:q309242
A:Superfamily: histo-blood group I transferase
C:Keywords: glycosyltransferase; hexosyltransferase; transmembrane protein

Query Match 73.5%; Score 1476.5; DB 2; Length 394;
Best Local Similarity 72.2%; Pred. No. 2.9e-116;
Matches 268; Conservative 41; Mismatches 47; Indels 15; Gaps 3;

QY 1 MNVKGVLMSLVSTVIVFWYTHSPGSLFWINPSKNPEVGSSIQGKMWLPRWFNN 60
Db 36 MNVKGVTLLMLIVSTVVVFWMEYV-----NRIPEVGENRQKDMWPFSEKN 83
QY 61 GYH--EEGDIDNEEKQKNEDE-SKLKLSDMFNPKRPREVYTMTKKAPVWEGTYNRAV 117
Db 84 GTHSYQENNVGRKKKKGNGCRIDIEPQLMDMFPNPNRDVLTVPWKAIVWEGYDAL 143
QY 118 LDNYAKAKITVGLITFVAVGRYIEHYLEEFITSAKNHFNMGHPVIFYLMDVDSMPLE 177
Db 144 LEKYATQKLTIVGLITFVAVGRYIEHYLEDFLESADMTFMVGRYIFYMIDTISMPYVH 203
QY 178 LGLPSRFKVPKIRPKKWDIISMFRKTIIGHIVAHIQHEWYPLFCMDVDVFODFGVE 237
Db 204 LNPILSLQVFIERSEKRWODISMFRKTIIGHIILAHIQHEYDFLCMDVDVFODFGVE 263
QY 238 TLGSEVALQAMWKKADPNDFYERRKESAAVIFPGCEDFYHAAIFGCTGYOANTIOE 297
Db 264 TLGQVALQAMWKKASPEKTYTERRELSAAVIFPGCEDFYHAAIFGCTGYHINTLRE 323
QY 298 CFKGLKDKRKNDIEAQMDESHLNKYPFLNKPRTKLSPCYCMDYHIGPADIKLVKMSQ 357
Db 324 CFKGLIDQKKHNDIEAQMDESHLNKPYFLNKNPRTKLSPCYCMDYDQIGLPSDIKSVKAWQ 383
QY 358 TKEYNVVARNV 368
Db 384 TKEYNLVRNV 394

RESULT 6
PC1120
fucosylgalactose alpha-N-acetylglucosaminyltransferase (EC 2.4.1.40) A2 allele [valide
N:Alternate names: histo-blood group A2 transferase
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 08-Sep-2000
C:Accession: PC1120
C:Yamamoto, F.; McNeill, P.D.; Hakomori, S.

```

Biochem. Biophys. Res. Commun. 187, 366-374, 1992

A>Title: Human histo-blood group A2 transferrase coded by A2 allele, one of the A subtype
A:Reference number: PC1120; MUID:q2392351
A:Accession: PC1120
C:Molecule type: DNA
A>Status: nucleic acid sequence not shown

A:Residues: 1-295 <YAM>
A:Cross-references: GB:S44054; NID:g255066; PION:AAB23167.1; PID:g255067
C:Superfamily: histo-blood group I transferase
C:Keywords: glycosyltransferase; hexosyltransferase

Query Match 32.8% Score 658; DB 2; Length 295:
Best Local Similarity 45.3%; Prod. No. 9,7e+48;
Matches 124; Conservative 50; Mismatches 98; Indels 2; Gaps 2;

Oy 94 RPEVATMKKKAPVVWECTYKRAVLADNYAAOKITVCGLTAVAGCYLIEHLLEPLTSANK 153
 |::|::||::||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 1 RKDYLVPRLPMLAPIWESTPNIDLKEGFRJONTIGTLTAIRKYVA-FLIKLTAEAK 59
Oy 154 HFMWGHPVIPTVMVDVSRRMPLIELGPILRSFKVEIKPKFQMODISMIRMKTGEHIAIH 213
 |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 60 HFMGCHRHRYHYVFPPDLQAALVRVTLLGTGRQLSVLFVARYKRMDYSMRMHIMSDPCERR 119
Oy 214 IQHEVDLPFCNDVDVDFYDKFGCVETLIGESVALOLAWMYKAUPNDEYEKKESAAYIPPG 273
 ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 120 FLSEVDYLACVDVDMERFDHGVELLDPLEFLTHRGFYSSREAFTEPRRQCAYIPKD 179
Oy 274 EGDFTYYHAALICGGTPTOVLNTICECFKGILDKKNIDEACHHDHSLNKTYLKPKTKI 333
 |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 180 EGDPFFLYLGFGFGSGVOEQRULTRACHCAMWDQANGIPAWHEDSHLNKYLIIHKRPVKL 239
Oy 334 SPEYCWDYH-TGLPADIKLVKMMSMQEKENVVN 366
 |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 240 SPETYLMDOOLLGWPAVLRKLRFTAARPHNHQAVRN 273

RESULT 7

Fucosylgalactose alpha-N-acetylglactosaminyltransferase (EC 2.4.1.40) Al allele [val]
A349933
NAlternate names: alpha-3-N-acetylglactosaminyltransferase; blood-group substance A e; histo-blood group A glycosyltransferase
C:Species: Homo sapiens (man)
C:Date: 18-Aug-2000 #sequence revision 18-Aug-2000 #extl_change 08-Sep-2000
A:Accession: A349933; S099933; SI3173; PC1164
R.Yamamoto, F.; Marken, J.; Tsuji, T.; White, T.; Clausen, H.; Hakomori, S.
J. Biol. Chem. 265, 1146-1151, 1990
A>Title: Cloning and characterization of cDNA complementary to human UDP-GalNAc 4-Epimerase
A:Reference number: A349933; MUID:90110098
A:Accession: A349933
A:Molecule type: mRNA
A:Residues: 1-353 <YAM1>
A:CROSS-references: GR:J05175; NID:g340077; PION:AAA36792.1; PID:g340078
R.Yamamoto, F.I.; Clausen, H.; White, T.; Marken, J.; Hakomori, S.L.
Nature 345, 229-233, 1990
A>Title: Molecular genetic basis of the histo-blood group ABO system.
A:Reference number: S099933; MUID:90238543
A:Accession: S099933
A>Status: Preliminary; nucleic acid sequence not shown; compared with conceptual
A:Molecule type: mRNA
A:Residues: 1-353 <YAM2>
R.Navaratnam, N.; Findlay, J.B.C.; Keen, J.N.; Watkins, W.M.
Biochem. J. 271, 93-98, 1990
A>Title: Purification, properties and partial amino acid sequence of the blood-group-A antigen.
A:Reference number: SI3173; MUID:91024951
A:Accession: SI3173
A>Status: Preliminary
A:Molecule type: protein
A:Residues: 7X, 65-77, 7S*, 76-77 <NAV>
R.Kominato, Y.; McNeill, P.D.; Yamamoto, M.; Russell, M.; Hakomori, S.; Yamamoto, F.
Biochem. Biophys. Res. Commun. 189, 154-164, 1992
A>Title: Animal histo-blood group ABO genes.

A. KOTTECHILLOU: NUMBER: 171164; MU11: 93080551

A; Molecule type: DNA

A; Molecule type: DNA

A; Kees Janes: 1-189-7808
c'; Super Family: histo-bl

c'; Superfamily: histo-blood group 1 transferase

| | | | | |
|---------------|--------|------------------|-------|-------------|
| Chiefly Match | 22.4%; | Score 449.5; | DB 2; | Length 189. |
| Chiefly Match | 46.4%; | Seed No. 179-30. | | |

| | |
|-----------------------|------------------------------------------------------|
| Best Local Similarity | 46.38; Pred. No. 1,78-302 |
| Matches | 87; Conservative 27; Mismatches 73; Indels 1; Gaps 1 |

| | | | | | | | | | |
|------------|-----|--------------|-----|------------|-----|--------|----|------|---|
| Mismatches | 87; | Conservative | 27; | Mismatches | 73; | Indels | 1; | Gaps | 1 |
|------------|-----|--------------|-----|------------|-----|--------|----|------|---|

0Y 161 VVVFVVVVDSKRPPLLEAASPLKSPFVKFKRKRKKKKODISMRKMTIGEHIVAHIQHEVDV 22
1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Dd 2 VIIIVVFVTIOPAAVPKRVITICTGROI.SVLIAFYAKRKQDVDSMRHMEMISDFCTERRFLISEVDY 61

2 VHYVFTTQIAVPRVTIGTOROI.SVIGVRAYKRWQVSMRKMMLSIDFCHRRFISHVDI 61

[illegible]

62 1.VCVDVIMFFRKHVCVELTPPLGTLHPGFYGSTKEAFYYEKRPQDAYIPKDEGDFYLL 12

cy 281 AATGGGTGTVVINITDPEFGKLEKKNDIEAQMIDESH_LNKYFLANKPTKLISPECMD 340
||| : || : || : || : || | ||| ||||||| : ||||| ||||| ||
tab 122 GTFPGSVQVEGRLETRACHQAMMVQANILEAVHIDESLNKYLLRKPKVLSPETLMD 180

122 G3FPGGVQRIITKACIQAMMVIQANGIEAVVHDESLNKYLLKHKPTKVLSP EYIWD 184

| | | |
|-----|---------------|-----|
| QY | 441 YH 101PA | 447 |
| | 1111 | |
| 10b | 182 QULJGWPJA | 189 |

[illegible]

RESULTS

histo-blood group transferase - crab-eating macaque (*Fragment 2*)
 histone H4 - Macaca mulatta (crab-eating macaque)

```

c; Date: 07-May-1993 #Sequence_revision 07-May-1993 #Text_change 07-May-1993
#Annotation_revision 07-May-1993

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Kojima, Y.; McNeill, P. D.; Yamamoto, M.; Russell, M.; Hakomori, S.; Yamamoto, F.; Yamamoto, T. *Journal of Neurochemistry* 1992, 59, 154-164.

A; Title: Animal histo-blood group ABO genes
Accession number: U01164; MIM: 934805

A; Accession: 101171

A. K. Sridhar: 1-189-A(K)M

| | | | | |
|--------------------|--------|-----------------|-------|-------------|
| Query Match | 22.48; | Score 449.5; | DB 2; | Length 189; |
| Percent Similarity | 46.39; | Prod NO 172-30; | | |

| Category | Count |
|--------------|-------|
| Matches | 87 |
| Conservative | 27 |
| Mismatches | 73 |
| Indels | 1 |
| Gaps | 1 |

161 VIFYIMVUDVSKMPLLEICPLRSFKVKIKPEKRWODISMMRMKTICGHVAHLOHEVIDF 220

1db 2 VHYVFTDQPAAVPRVALGTGKQLSVLGVRAYKKWQVSMKRMEMISDFCEQRFLSEVDY 61

Qy 221 LFCMDVGVGVGDKRGVFETLGGESVAGLQAMWYKADPNDFTYERRKESAAVLPFGEGDFFVH 280
+ + + + + : + + + + +
Db 62 LVEVDVDMDEFRHHGVETLTPLTGLPAEYGSSEAFETYERRQSQAALPKRQGFDFYL 120

62 ~~NCVAVIMDEFRIHVGVELLPPLFGLHFAFGSSKFAFIKRRQSGQALPRNDIGDFILP~~ 124

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0Y      281 AATGGGTTCVLTNTTGTCTKGLKKRKNDDAQMHDPSHLNRYFLTNKPTKILSPFYCMD 340
      111 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
10b     122 GTFGGSGVGEVQKLTAKCHQAMMVQANGTAAVMHDSHLNKYTLKRKPTKVLSPFYAMD 180

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122 GFFFGSSVGEVQKLTFRACHQAMMVIDQANGTAAVWIMDESILNKYLIARKNPAAVLSPEIEMD 184

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| QY | 441 YH | ICLPA | 347 |
| | : | : | : |
| IB | 182 QULCMA | 189 | |

681 VAMPIRO ZH 191

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Search completed: November 5, 2001, 15:19:14

Search completed: November 5, 2001, 15:19:14
Job time: 8442 sec

Job time: 84.42 sec